

AMENDMENTS TO THE CLAIMS

1. - 35. (canceled)

36. (currently amended) A method of ~~determining whether a human has identifying~~
~~a human having~~ an increased risk for developing positive autoantibody rheumatoid factor (RF+) Rheumatoid Arthritis (RA), comprising testing nucleic acid from said human to detect the nucleotide content ~~for the presence or absence~~ of a single nucleotide polymorphism (SNP) at position 101 of SEQ ID NO: 5502 or its complement, wherein a G/G genotype at position 101 of SEQ ID NO: 5502 or a C/C genotype at position 101 of its complement indicates said human has an increased risk for developing RF+ RA.

37. - 38. (canceled)

39. (currently amended) The method of claim 36 in which SEQ ID NO: 5502 is contained within the genomic sequence of the TRIP (TRAF interacting protein) gene as shown by SEQ ID NO: 1688.

40. (previously presented) The method of claim 36 in which the SNP is located at position 6497 of SEQ ID NO: 1688.

41. (previously presented) The method of claim 36 in which said nucleic acid is a nucleic acid extract from a biological sample of said human.

42. (previously presented) The method of claim 41 in which said biological sample is blood, saliva, or buccal cells.

43. (previously presented) The method of claim 36, wherein said testing step comprises nucleic acid amplification.

44. (previously presented) The method of claim 36 in which the testing is performed by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 6629, SEQ ID NO: 6630, and SEQ ID NO: 6631.

45. (previously presented) The method of claim 36 in which the testing is performed by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

46. - 55. (canceled)

56. (currently amended) A method of determining a human's risk for developing positive autoantibody rheumatoid factor (RF+) Rheumatoid Arthritis (RA), comprising testing nucleic acid from said human to detect the nucleotide content ~~for the presence or absence~~ of a single nucleotide polymorphism (SNP) at position 101 of SEQ ID NO: 5502 or its complement, wherein a G/G genotype at position 101 of SEQ ID NO:5502 or a C/C genotype at position 101 of its complement indicates said human has an increased risk for developing RF+ RA, or A at position 101 of SEQ ID NO:5502 or T at its complement indicates said human has a decreased risk for developing RF+ RA.

57. - 58. (canceled)

59. (previously presented) The method of claim 56 in which SEQ ID NO: 5502 is contained within the genomic sequence of the TRIP gene as shown by SEQ ID NO: 1688.

60. (previously presented) The method of claim 56 in which the SNP is located at position 6497 of SEQ ID NO: 1688.

61. (previously presented) The method of claim 56 in which said nucleic acid is a nucleic acid extract from a biological sample of said human.

62. (previously presented) The method of claim 61 in which said biological sample is blood, saliva, or buccal cells.

63. (previously presented) The method of claim 56, wherein said testing step comprises nucleic acid amplification.

64. (previously presented) The method of claim 56 in which the testing is performed by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 6629, SEQ ID NO: 6630, and SEQ ID NO: 6631.

65. (previously presented) The method of claim 56 in which the testing is performed by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

66. (currently amended) A method of determining whether a human has ~~identifying a human having~~ a decreased risk for developing positive autoantibody rheumatoid factor (RF+) Rheumatoid Arthritis (RA), comprising testing nucleic acid from said human to detect the nucleotide content ~~for the presence or absence~~ of a single nucleotide polymorphism (SNP) at position 101 of SEQ ID NO: 5502 or its complement, wherein A at position 101 of SEQ ID NO: 5502 or T at its complement indicates said human has a decreased risk for developing RF+ RA.

67. (previously presented) The method of claim 66 in which SEQ ID NO: 5502 is contained within the genomic sequence of the TRIP gene as shown by SEQ ID NO: 1688.

68. (previously presented) The method of claim 66 in which the SNP is located at position 6497 of SEQ ID NO: 1688.

69. (previously presented) The method of claim 66 in which said nucleic acid is a nucleic acid extract from a biological sample of said human.

70. (previously presented) The method of claim 69 in which said biological sample is blood, saliva, or buccal cells.

71. (previously presented) The method of claim 66, wherein said testing step comprises nucleic acid amplification.

72. (previously presented) The method of claim 66 in which the testing is performed by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 6629, SEQ ID NO: 6630, and SEQ ID NO: 6631.

73. (previously presented) The method of claim 66 in which the testing is performed by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

74. (currently amended) A method of determining whether a human has ~~identifying a human having~~ a decreased risk for developing positive autoantibody rheumatoid factor (RF+) Rheumatoid Arthritis (RA), comprising testing nucleic acid from said human to detect the nucleotide content ~~for the presence or absence~~ of single nucleotide polymorphism (SNP) hCV163035, wherein A at the SNP based on the sequence orientation of SEQ ID NO:5502 or T at the SNP based on the sequence orientation of the complement of SEQ ID NO:5502 indicates said human has a decreased risk for developing RF+ RA.

75. (currently amended) A method of determining whether a human has an increased ~~identifying a human having a decreased~~ risk for developing positive autoantibody rheumatoid factor (RF+) Rheumatoid Arthritis (RA), comprising testing nucleic acid from said human to detect the nucleotide content ~~for the presence or absence~~ of single nucleotide

polymorphism (SNP) hCV163035, wherein a G/G genotype at the SNP based on the sequence orientation of SEQ ID NO:5502 or a C/C genotype at the SNP based on the sequence orientation of the complement of SEQ ID NO:5502 indicates said human has an increased risk for developing RF+ RA.

76. (previously presented) The method of claim 61, further comprising preparing said nucleic acid extract from said biological sample prior to said testing step.

77. (previously presented) The method of claim 76, further comprising obtaining said biological sample from said human prior to said preparing step.

78. (previously presented) The method of claim 63, wherein said nucleic acid amplification is carried out by polymerase chain reaction.

79. (currently amended) The method of claim 36, further comprising correlating the presence of said G/G genotype or said C/C genotype with an increased risk for developing positive autoantibody rheumatoid factor (RF+) Rheumatoid Arthritis (RA) coronary stenosis.

80. (previously presented) The method of claim 79, wherein said correlating step is performed by computer software.

81. (currently amended) The method of claim 36, further comprising correlating the absence of said G/G genotype or said C/C genotype with no increased risk for developing positive autoantibody rheumatoid factor (RF+) Rheumatoid Arthritis (RA) coronary stenosis.

82. (previously presented) The method of claim 81, wherein said correlating step is performed by computer software.

83. (currently amended) The method of claim 66, further comprising correlating the presence of said A or said T with a decreased risk for developing positive autoantibody rheumatoid factor (RF+) Rheumatoid Arthritis (RA) coronary stenosis.

84. (previously presented) The method of claim 83, wherein said correlating step is performed by computer software.